

## SEQUENCE LISTING

<110> THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
LEE, Se-Jin  
ESQUELA, Aurora F.

<120> METHODS OF DETECTING LIVER CELLS EXPRESSING GROWTH DIFFERENTIATION FACTOR-12

<130> JHU1220-4

<140> US 09/361,655  
<141> 1999-07-27

<150> US 08/765,662  
<151> 1997-04-28

<150> PCT/ US95/08745  
<151> 1995-07-12

<150> US 08/274,215  
<151> 1994-07-13

<160> 14

<170> PatentIn version 3.1

<210> 1  
<211> 34  
<212> DNA  
<213> Artificial sequence

<220>  
<223> PCR primer

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> n = inosine

<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> n is any nucleotide

<220>  
<221> misc\_feature  
<222> (26)..(26)  
<223> n = inosine

<220>  
<221> misc\_feature  
<222> (29)..(29)  
<223> n = inosine

<400> 1  
ccggaattcg gntggmgnva tggrrtnrtnt aycc

<210> 2  
<211> 33  
<212> DNA

```

<213> Artificial sequence

<220>
<223> PCR primer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 2
ccggaattcr cansrcanc ynwcnaclnry cat

```

33

```

<210> 3
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

```

```

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 3
ccggaattcr cansrcrant snygnacnry cat

```

33

```

<210> 4
<211> 33
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> PCR primer

```

```

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

```

```

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

```

```

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

```

```

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

```

```

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

```

```

<400> 4
ccggaattcr cansrcrant snwcnaclnry cat

```

33

```

<210> 5
<211> 33
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> PCR primer

```

```

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

```

```

<220>

```

```

<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 5
ccggaattcr cansrcrant snbtnacnry cat 33

<210> 6
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 6
ccggaattcr cansrcrang mnnygnacnry cat 33

<210> 7

```

```
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 7
ccggaattcr cansrcang mnwcnacnry cat
```

33

```
<210> 8
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
```

```

<222> (25)..(25)
<223> n = inosine

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 8
ccggaattcr canscrcanm gnygnacnry cat

```

33

```

<210> 9
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

```

```

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 9
ccggaattcr canscrcanm gnwcnaenry cat

```

33

```

<210> 10
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n = inosine

```

```

<220>
<221> misc_feature
<222> (19)..(19)
<223> n = inosine

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = inosine

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = inosine

<400> 10
ccggaattcr cansrcanm gnbtnacnry cat 33

<210> 11
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(357)
<223>

<400> 11
cg gcc agg agg acc ccc acc tgt gag cct gcg acc ccc tta tgt 48
Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu Cys
1 5 10 15
tgc agg cga gac cat tac gta gac ttc cag gaa ctg gga tgg cg gac 96
Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg Asp
20 25 30

tgg ata ctg cag ccc gag ggg tac cag ctg aat tac tgc agt ggg cag 144
Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly Gln
35 40 45

tgc cct ccc cac ctg gct ggc agc cca ggc att gct gcc tct ttc cat 192
Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe His
50 55 60

tct gcc gtc ttc agc ctc ctc aaa gcc aac aat cct tgg cct gcc agt 240
Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala Ser
65 70 75 80

acc tcc tgt tgt gtc cct act gcc cga agg ccc ctc tct ctc tac 288
Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu Tyr
85 90 95

ctg gat cat aat ggc aat gtg gtc aag acg gat gtg cca gat atg gtg 336

```

Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met Val  
 100 105 110

gtg gag gcc tgt ggc tgc agc tag 360  
 Val Glu Ala Cys Gly Cys Ser  
 115

<210> 12  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu Cys  
 1 5 10 15

Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg Asp  
 20 25 30

Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly Gln  
 35 40 45

Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe His  
 50 55 60

Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala Ser  
 65 70 75 80

Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu Tyr  
 85 90 95

Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met Val  
 100 105 110

Val Glu Ala Cys Gly Cys Ser  
 115

<210> 13  
 <211> 2419  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (218)..(1267)  
 <223>

<400> 13  
 gagctgtgag ggtcaagcac agctatccat cagatgatct actttcagcc ttccctgagtc 60  
 ccagacaata gaagacaggt ggctgtaccc ttggccaagg gttagtgtgg cagtggtgtc 120

|  |                         |     |     |
|--|-------------------------|-----|-----|
| tgctgtcaact gtgccctcat tggcccccag caatcagact caacagacgg agcaactgcc |                         | 180 |     |
| atccgaggct cctgaaccag ggccattcac caggagc atg cggtt ctc cct gat gtc | Met Arg Leu Pro Asp Val | 235 |     |
| 1  | 5                       |     |     |
| cag ctc tgg ctg gtg ctg tgg gca ctg gtg cga gca cag ggg aca        |                         | 283 |     |
| Gln Leu Trp Leu Val Leu Leu Trp Ala Leu Val Arg Ala Gln Gly Thr    |                         |     |     |
| 10   | 15                      | 20  |     |
| ggg tct gtg tgt ccc tcc tgt ggg ggc tcc aaa ctg gca ccc caa gca    |                         | 331 |     |
| Gly Ser Val Cys Pro Ser Cys Gly Gly Ser Lys Leu Ala Pro Gln Ala    |                         |     |     |
| 25   | 30                      | 35  |     |
| gaa cga gct ctg gtg ctg gag cta gcc aag cag caa atc ctg gat ggg    |                         | 379 |     |
| Glu Arg Ala Leu Val Leu Glu Leu Ala Lys Gln Gln Ile Leu Asp Gly    |                         |     |     |
| 40   | 45                      | 50  |     |
| ttg cac ctg acc agt cgt ccc aga ata act cat cct cca ccc cag gca    |                         | 427 |     |
| Leu His Leu Thr Ser Arg Pro Arg Ile Thr His Pro Pro Pro Gln Ala    |                         |     |     |
| 55   | 60                      | 65  | 70  |
| gcg ctg acc aga gcc ctc cgg aga cta cag cca ggg agt gtg gct cca    |                         | 475 |     |
| Ala Leu Thr Arg Ala Leu Arg Arg Leu Gln Pro Gly Ser Val Ala Pro    |                         |     |     |
| 75   | 80                      | 85  |     |
| ggg aat ggg gag gag gtc atc agc ttt gct act gtc aca gac tcc act    |                         | 523 |     |
| Gly Asn Gly Glu Glu Val Ile Ser Phe Ala Thr Val Thr Asp Ser Thr    |                         |     |     |
| 90   | 95                      | 100 |     |
| tca gcc tac agc tcc ctg ctc act ttt cac ctg tcc act cct cgg tcc    |                         | 571 |     |
| Ser Ala Tyr Ser Ser Leu Leu Thr Phe His Leu Ser Thr Pro Arg Ser    |                         |     |     |
| 105  | 110                     | 115 |     |
| cac cac ctg tac cat gcc cgc ctg tgg ctg cac gtg ctc ccc acc ctt    |                         | 619 |     |
| His His Leu Tyr His Ala Arg Leu Trp Leu His Val Leu Pro Thr Leu    |                         |     |     |
| 120  | 125                     | 130 |     |
| cct ggc act ctt tgc ttg agg atc ttc cga tgg gga cca agg agg agg    |                         | 667 |     |
| Pro Gly Thr Leu Cys Leu Arg Ile Phe Arg Trp Gly Pro Arg Arg Arg    |                         |     |     |
| 135  | 140                     | 145 | 150 |
| cgc caa ggg tcc cgc act ctc ctg gct gag cac cac atc acc aac ctg    |                         | 715 |     |
| Arg Gln Gly Ser Arg Thr Leu Leu Ala Glu His His Ile Thr Asn Leu    |                         |     |     |
| 155  | 160                     | 165 |     |
| ggc tgg cat acc tta act ctg ccc tct agt ggc ttg agg ggt gag aag    |                         | 763 |     |
| Gly Trp His Thr Leu Thr Leu Pro Ser Ser Gly Leu Arg Gly Glu Lys    |                         |     |     |
| 170  | 175                     | 180 |     |
| tct ggt gtc ctg aaa ctg caa cta gac tgc aga ccc cta gaa ggc aac    |                         | 811 |     |
| Ser Gly Val Leu Lys Leu Gln Leu Asp Cys Arg Pro Leu Glu Gly Asn    |                         |     |     |
| 185  | 190                     | 195 |     |
| agc aca gtt act gga caa ccg agg cgg ctc ttg gac aca gca gga cac    |                         | 859 |     |
| Ser Thr Val Thr Gly Gln Pro Arg Arg Leu Leu Asp Thr Ala Gly His    |                         |     |     |
| 200  | 205                     | 210 |     |
| cag cag ccc ttc cta gag ctt aag atc cga gcc aat gag cct gga gca    |                         | 907 |     |
| Gln Gln Pro Phe Leu Glu Leu Lys Ile Arg Ala Asn Glu Pro Gly Ala    |                         |     |     |

| 215   | 220 | 225 | 230  |
|---|-----|-----|------|
| ggc cg gcc agg agg acc ccc acc tgt gag cct gcg acc ccc tta<br>Gly Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu             |     |     | 955  |
| 235   | 240 | 245 |      |
| tgt tgc agg cga gac cat tac gta gac ttc cag gaa ctg gga tgg cgg<br>Cys Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg        |     |     | 1003 |
| 250   | 255 | 260 |      |
| gac tgg ata ctg cag ccc gag ggg tac cag ctg aat tac tgc agt ggg<br>Asp Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly        |     |     | 1051 |
| 265   | 270 | 275 |      |
| cag tgc cct ccc cac ctg gct ggc agc cca ggc att gct gcc tct ttc<br>Gln Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe        |     |     | 1099 |
| 280   | 285 | 290 |      |
| cat tct gcc gtc ttc agc ctc ctc aaa gcc aac aat cct tgg cct gcc<br>His Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala        |     |     | 1147 |
| 295   | 300 | 305 | 310  |
| agt acc tcc tgt tgt gtc cct act gcc cga agg ccc ctc tct ctc ctc<br>Ser Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu        |     |     | 1195 |
| 315   | 320 | 325 |      |
| tac ctg gat cat aat ggc aat gtg gtc aag acg gat gtg eca gat atg<br>Tyr Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met        |     |     | 1243 |
| 330   | 335 | 340 |      |
| gtg gtg gag gcc tgt ggc tgc agc tagcaagagg acctggggct ttggagtgaa<br>Val Val Glu Ala Cys Gly Cys Ser                                       |     |     | 1297 |
| 345   | 350 |     |      |
| gagaccaaga tgaagtttcc cagggcacagg gcatctgtga ctggaggcat cagattcctg<br>atcccacaccc caaccacaaca accacctggc aatatgactc acttgacccc tatgggaccc |     |     | 1357 |
| aatgggcac tttcttgtct gagactctgg cttattccag gttggctgat gtgttggag<br>atggtaaag cgtttcttct aaaggggtct acccagaaaag catgatttcc tgccctaagt      |     |     | 1417 |
| cctgtgagaa gatgtcaggg actagggagg gagggaggaa aggcagagaa aaattactta<br>gcctctccca agatgaaaaa gtcctcaagt gaggggaggaa ggaaggcagat agatggtcca  |     |     | 1477 |
| gcaggcttga agcagggtaa gcaggctggc ccaggtaag ggctgtttagt gtttttttt<br>ggaaggtaa gagggagatg ggcaaggcgc tgagggaggaa tgcttagggg accccccagaa    |     |     | 1537 |
| acaggagtca ggaaaatgag gcactaagcc taagaagtgc cctggggggat<br>aggacccact gggagacaag catttatact ttctttcttc ttttttattt tttttttttt              |     |     | 1657 |
| gagtctcgct ctgtcaccag gctggagtgc agtgacacga tcttggctca ctgcaaccc<br>cgtctctgg gttcaagtga ttcttctgcc tcagccccc gagcagctgg gattacaggc       |     |     | 1897 |
| gccccactaat ttttgtattc ttagtagaaa cgaggttca acatgttggc caggatggtc<br>tcaatcttctt gaccttcttga tccacccgac ttggccccc gaagtgtatga gattataggc  |     |     | 2017 |
| 2077  |     |     |      |
| tcaatcttctt gaccttcttga tccacccgac ttggccccc gaagtgtatga gattataggc<br>2137   |     |     |      |

|   |      |
|---|------|
| gtgagccacc gcgcctggct tatactttct taataaaaag gagaaagaaa atcaacaaat | 2197 |
| gtgagtcata aagaagggtt agggtgatgg tccagagcaa cagttttca agtgtactct  | 2257 |
| gtaggctct gggaggtccc tttcagggg tgtccacaaa gtcaaagcta ttttcataat   | 2317 |
| aatactaaca tgttatgc ctgtgaatt ctcattatct taaaattgta ttgtggagtt    | 2377 |
| ttccagaggc cggtgtgacat gtgattacat catcttctg ac                    | 2419 |

<210> 14  
 <211> 350  
 <212> PRT  
 <213> Homo sapiens

<400> 14

|   |   |    |    |
|---|---|----|----|
| Met Arg Leu Pro Asp Val Gln Leu Trp Leu Val Leu Leu Trp Ala Leu |   |    |    |
| 1   | 5 | 10 | 15 |

|   |    |    |
|---|----|----|
| Val Arg Ala Gln Gly Thr Gly Ser Val Cys Pro Ser Cys Gly Gly Ser |    |    |
| 20  | 25 | 30 |

|   |    |    |
|---|----|----|
| Lys Leu Ala Pro Gln Ala Glu Arg Ala Leu Val Leu Glu Leu Ala Lys |    |    |
| 35  | 40 | 45 |

|   |    |    |
|---|----|----|
| Gln Gln Ile Leu Asp Gly Leu His Leu Thr Ser Arg Pro Arg Ile Thr |    |    |
| 50  | 55 | 60 |

|   |    |    |    |
|---|----|----|----|
| His Pro Pro Pro Gln Ala Ala Leu Thr Arg Ala Leu Arg Arg Leu Gln |    |    |    |
| 65  | 70 | 75 | 80 |

|   |    |    |
|---|----|----|
| Pro Gly Ser Val Ala Pro Gly Asn Gly Glu Glu Val Ile Ser Phe Ala |    |    |
| 85  | 90 | 95 |

|   |     |     |
|---|-----|-----|
| Thr Val Thr Asp Ser Thr Ser Ala Tyr Ser Ser Leu Leu Thr Phe His |     |     |
| 100   | 105 | 110 |

|   |     |     |
|---|-----|-----|
| Leu Ser Thr Pro Arg Ser His His Leu Tyr His Ala Arg Leu Trp Leu |     |     |
| 115   | 120 | 125 |

|   |     |     |
|---|-----|-----|
| His Val Leu Pro Thr Leu Pro Gly Thr Leu Cys Leu Arg Ile Phe Arg |     |     |
| 130   | 135 | 140 |

|   |     |     |     |
|---|-----|-----|-----|
| Trp Gly Pro Arg Arg Arg Gln Gly Ser Arg Thr Leu Leu Ala Glu |     |     |     |
| 145   | 150 | 155 | 160 |

|   |     |     |
|---|-----|-----|
| His His Ile Thr Asn Leu Gly Trp His Thr Leu Thr Leu Pro Ser Ser |     |     |
| 165   | 170 | 175 |

Gly Leu Arg Gly Glu Lys Ser Gly Val Leu Lys Leu Gln Leu Asp Cys  
 180 185 190

Arg Pro Leu Glu Gly Asn Ser Thr Val Thr Gly Gln Pro Arg Arg Leu  
 195 200 205

Leu Asp Thr Ala Gly His Gln Gln Pro Phe Leu Glu Leu Lys Ile Arg  
 210 215 220

Ala Asn Glu Pro Gly Ala Gly Arg Ala Arg Arg Arg Thr Pro Thr Cys  
 225 230 235 240

Glu Pro Ala Thr Pro Leu Cys Cys Arg Arg Asp His Tyr Val Asp Phe  
 245 250 255

Gln Glu Leu Gly Trp Arg Asp Trp Ile Leu Gln Pro Glu Gly Tyr Gln  
 260 265 270

Leu Asn Tyr Cys Ser Gly Gln Cys Pro Pro His Leu Ala Gly Ser Pro  
 275 280 285

Gly Ile Ala Ala Ser Phe His Ser Ala Val Phe Ser Leu Leu Lys Ala  
 290 295 300

Asn Asn Pro Trp Pro Ala Ser Thr Ser Cys Cys Val Pro Thr Ala Arg  
 305 310 315 320

Arg Pro Leu Ser Leu Leu Tyr Leu Asp His Asn Gly Asn Val Val Lys  
 325 330 335

Thr Asp Val Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser  
 340 345 350